Atty Dkt. No.: TGEN-001 USSN: 09/471,703

AMENDMENTS

IN THE CLAIMS

- 1. -- 68. (Canceled).
- 69. (Currently Amended) A method for determining the identity of a polymorphic nucleotide in a target sequence having at least two known variant nucleotides at a site, comprising:

performing a primer extension reaction with the target sequence using an extension reaction mixture comprising:

a primer that specifically hybridizes to the target sequence such that there is a one or more nucleotide gap between the 3' terminus end of the primer and is one or more nucleotides 5' of a the variant nucleotide of the polymorphic site of the target sequence at the polymorphic site, and

a mixture of a plurality of deoxyribonucleoside triphosphates (dNTPs) or ribonucleoside triphosphates (rNTPs), where the plurality mixture of dNTPs or rNTPs provides for at least one nucleotide extension of the primer when hybridized to a target sequence having either of the two variant nucleotides at the polymorphic site, wherein the mixture excludes a dNTP or rNTP complementary to one of said variant nucleotides of the polymorphic site, and wherein the dNTPs or rNTPs in the mixture are not detectably labeled or modified, and

wherein the extension reaction is performed in the absence of a dideoxynucleoside triphosphate (ddNTP); and

analyzing reaction primer extension products of said extension reaction;

wherein the length of the primer extension products is indicative of the identity of the variant nucleotides at the polymorphic site.

70. (Canceled)

71. (Currently Amended) The method of claim 69, wherein the primer hybridizes to the target sequence such that there is a gap of at least two nucleotides between the 3' terminus of the primer

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and the variant nucleotide of the polymorphic of the target sequence its 3' end is 2 or more nucleotides 5' of the variant nucleotide.

- 72. (Previously Added) The method of claim 69, wherein said analyzing comprises determining the length of said reaction products.
- 73. (Previously Added) The method of claim 69, wherein said analyzing comprises performing a technique selected from the group consisting of chromatography, capillary electrophoresis, microfluidic analysis, and slab gel electrophoresis.
- 74. (Previously Added) The method of claim 69, wherein said analyzing comprises performing high performance liquid chromatography.
- 75. (Previously Added) The method of claim 69, wherein said analyzing comprises performing capillary electrophoresis.
- 76. (Previously Added) The method of claim 69, wherein said analyzing reaction products comprises determining the identity of a nucleotide incorporated in a reaction product.
- 77. (Previously Added) The method of claim 69, wherein said analyzing comprises use of an intercalating agent.
- 78. (Previously Added) The method of claim 77, wherein the intercalating agent is ethidium bromide.
- 79. (Previously Added) The method of claim 77, wherein the intercalating agent is an unsymmetrical cyanine dye.
- 80. (Previously Added) The method of claim 69, wherein said analyzing comprises use of slab electrophoresis and ultraviolet light.

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- 81. (Previously Added) The method of claim 69, wherein the reaction products are detected using slab electrophoresis and a DNA-binding dye.
- 82. (Previously Added) The method of claim 69, wherein the target sequence comprises a biallelic marker associated with genetic disorders.
- 83. (Previously Added) The method of claim 69, wherein the target sequence is present in a sample obtained from a diploid organism.
- 84. (Currently Amended) A method for screening a DNA sample for a plurality of target sequences having at least two known variants, comprising:

contacting a sample comprising a plurality of known target sequences with an extension reaction mixture to produce primer extension reaction products, the extension reaction mixture comprising

a primer that specifically hybridizes to a target sequence of interest such that there is a one or more nucleotide gap between the 3' end terminus of the primer and is at least one nucleotide 5' of a the variant nucleotide of the polymorphic site of the target sequence, and

a plurality <u>mixture</u> of deoxyribonucleoside triphosphates (dNTPs) or ribonucleoside triphosphates (rNTPs), where the plurality of dNTPs or rNTPs in the mixture provide for at least one nucleotide extension of the primer when hybridized to a target sequence having either of the two variant nucleotides, the mixture excluding a dideoxynucleoside triphosphate (ddNTP) and further excluding a dNTP or rNTP complementary to one of said variant nucleotides of the SNP, wherein the dNTPs or rNTPs in the mixture are not detectably labeled or modified; and analyzing the reaction <u>primer extension</u> products of each extension reaction;

wherein the length of the primer extension products is indicative of the identity of the variant nucleotides at the polymorphic site.

- 85. (Previously Added) The method of claim 84, wherein the target sequence is associated with genetic disorders.
 - 86. (Previously Added) The method of claim 84, wherein the sample is from a diploid organism.

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87. (Currently Amended) The method of claims 84, wherein the extension reaction mixture comprises at least two a plurality of different primers, which primers specifically hybridize to different target sequences, wherein each primer is of a length or sequence such that extension products of the different primers can be distinguished one from another.

88. (Previously Added) The method of claim 87, wherein the different primers are of different lengths.